Identification over Multiple Databases

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***Abstract*—The tradeoff between storage and identification rates for multiple databases is investigated from an information theoretic perspective. In the assumed model, noisy observations of feature vectors of two distinct groups, called the ancestors, are compressed and stored in two separate databases. When queried with a noisy observation of a (possibly random) function of two randomly selected ancestors (one from each group), the system is required to correctly identify the ancestors with high probability. Single-letter inner and outer bounds are presented on the set of achievable rate points, which identify a tradeoff between the compression rates and the identification rate region: the lower the compression rates for storage, the larger the rate region achievable for identification.**

I. Introduction

With the technological advances and the decreasing cost of memory devices, processing huge data sets has emerged as a fundamental research problem in various applications, such as information retrieval over the Internet, managing raw data from large sensor networks, or storing and processing biometric data. Various techniques have been developed for efficient management of these large databases, and in most cases, these techniques are specialized to the structure of the underlying data. However, it is important to develop fundamental bounds on data storage requirements to provide benchmarks for the memory requirements of these systems.

In this work we address these fundamental bounds by considering storage and identification over multiple databases. We assume that there are two groups of entries that are compressed and stored in two separate databases in an enrollment phase (extension to multiple databases is possible using the techniques in this paper). Each query is assumed to be a (possibly random) function of two entries, one entry from each database. The user of the database wants to identify the ancestors of this query over the two databases.

One application of this model is the *parent identification problem* using biometric databases, which may contain information from measurements of various biological features such as protein sequences, microarray gene expressions or metabolic pathways. We assume that the considered features are hereditary. In the *enrollment* phase, noisy measurements of the feature vectors of a population are captured, and the compressed version of each measurement is stored in one of the two databases according to the individual's gender. We then want to identify the parents of a child, based on a noisy observation of the child's feature vector, among the individuals stored in the two databases.

The identification capacity for a single biometric database is characterized in [2] as the mutual information between the noisy enrollment distribution and the noisy query distribution. In [2], the enrollment data is assumed to be stored directly in the database. However, to improve the efficiency of the identification process in the storage device, it may be desirable to store only a compressed version of the observed feature vectors. Under this model, the identification capacity/storage tradeoff is characterized in [3] and independently in [4]. While [3], formulating the problem in the pattern recognition context, also considers compression of the observed feature vectors, [4] studies a multi-stage identification system.

Here, we propose fundamental information theoretic bounds on the performance of identification systems over multiple databases in terms of the storage requirements and the number of individuals that can be identified. Following the previous work in [2]-[3] the entries are modeled as being independent and identically distributed (i.i.d.). This i.i.d. assumption is common in statistical modeling of DNA sequences [5], but more involved models are required for better performance. We model the reproduction process as a multiple access channel whose inputs are the feature vectors of the ancestors and the output is the child's feature vector. For the biometric applications, this channel might model the random cross-overs or the point mutations that occur during reproduction.

As we will see below, this problem can be considered as a combination of multi-terminal source and channel coding problems. Using techniques from multi-user information theory, we provide single letter inner and outer bounds on the set of achievable compression and identification rates.

The rest of the paper is organized as follows. We introduce the system model and the necessary definitions in Section II. The main result of the paper is presented in Section III, and its proof is given in Section IV. Section V concludes the paper.

II. System Model

We assume that there are two main groups in a population, which we generically name as 'male' and 'female'. Each group is characterized by an underlying probability distribution. The feature vectors of the males and the females in the population are denoted by $\{X_1^n(m_1)\}_{m_1=1}^{M_1}$ and $\{X_2^n(m_2)\}_{m_2=1}^{M_2}$,

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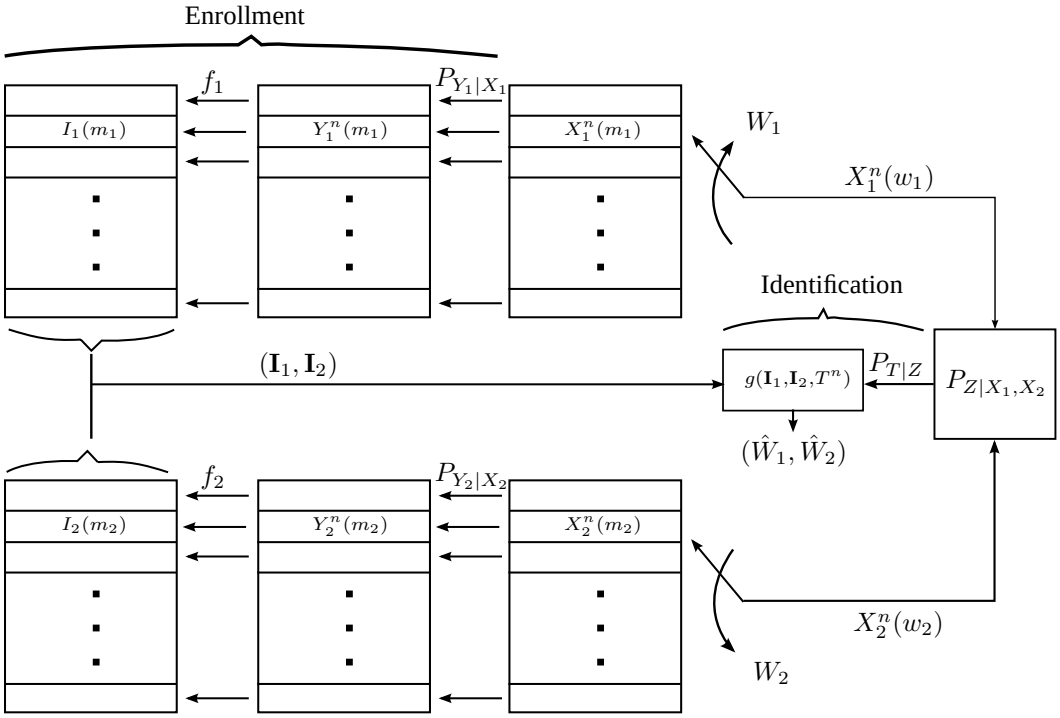

Fig. 1. The illustration of the enrollment and identification processes over two databases.

respectively. See Fig. 1 for an illustration of the system model. The underlying assumption is that the feature vectors are i.i.d. according to a probability distribution specific to each group. We have, for $j = 1, 2$ and $1 \leq m_j \leq M_j$, $P[X_j^n(m_j) = x_j^n] = \prod_{i=1}^n P_{X_j}(x_{ji})$, over the finite feature alphabets $\mathcal{X}_j$.

We assume that we have separate databases for the males and the females in the population. The databases are formed by an enrollment phase, in which the noisy version of the feature vector of an individual is observed and recorded to the corresponding database. We denote the observed noisy feature vectors by $Y_1^n(m_1)$ for males and $Y_2^n(m_2)$ for females, which are assumed to be the outputs of the corresponding discrete memoryless channel (DMC), which might be different for males and females. The DMCs are characterized by $P_{Y_1|X_1}$ and $P_{Y_2|X_2}$ for males and females, respectively, where $\mathcal{Y}_i$, $i = 1, 2$, are the finite observation alphabets. We have

$$P[Y_j^n(m_j) = y_j^n | X_j^n(m_j) = x_j^n] = \prod_{i=1}^n P_{Y_j|X_j}(y_{ji}|x_{ji}),$$

for $j = 1, 2$ and $1 \leq m_j \leq M_j$.

In the enrollment phase, each entry is compressed before it is recorded to the database, and only the compressed descriptions of the observed feature vectors are stored in the database. We consider two distinct deterministic functions for compression of each group: $f_j : \mathcal{Y}_j^n \to \mathcal{L}_j = \{1, \ldots, L_j\}$, for $j = 1, 2$, where $\mathcal{L}_j$ denotes the index set for the compressed observation vectors. We denote the index for entry $m_j \in \{1, \ldots, M_j\}$ as $I_j(m_j) = f_j(Y_j^n(m_j))$. These indices refer to n-length codewords of two separate codebooks of size L_j, $j = 1, 2$.

In the identification phase, W_1 and W_2 are chosen independent of each other and the database entries, and uniformly over the sets $\mathcal{M}_1 = \{1, \ldots, M_1\}$ and $\mathcal{M}_2 = \{1, \ldots, M_2\}$, respectively. The realizations are not known to the user of the database.

Now, consider an individual whose feature vector is derived from those of W_1 and W_2 through a DMC characterized by $P_{Z|X_1,X_2}$ with finite alphabet $\mathcal{Z}$, that is,

$$\begin{aligned} P[Z^n = z^n | X_1^n(W_1) = & x_1^n, X_2^n(W_2) = x_2^n] \\ &= \prod_{i=1}^n P_{Z|X_1,X_2}(z_i|x_{1i}, x_{2i}), \quad (1) \end{aligned}$$

where $Y_j^n - X_j^n - Z^n$ form Markov chains for $j = 1, 2$. The user of the database observes a noisy version of the feature vector Z^n of the individual corrupted by the DMC $P_{T|Z}$ with finite output alphabet $\mathcal{T}$, where $P[T^n = t^n | Z^n = z^n] = \prod_{i=1}^n P_{T|Z}(t_i|z_i)$.

Overall, the joint distribution of the random variables in the system is given by

$$P_{X_1,X_2,Y_1,Y_2,Z,T} = P_{X_1} P_{X_2} P_{Y_1|X_1} P_{Y_2|X_2} P_{Z|X_1,X_2} P_{T|Z}. \quad (2)$$

The user wants to identify W_1 and W_2, the two parents (ancestors) of the observed individual from each database by using the noisy observation vector T^n and the entries of the two databases $\{I_j(m_j)\}_{m_j=1}^{M_j}$, $j = 1, 2$.

The identification function is defined as $g : \mathcal{L}_1^{M_1} \times \mathcal{L}_2^{M_2} \times \mathcal{T}^n \to \mathcal{M}_1 \times \mathcal{M}_2$, and the corresponding estimates are denoted by $(\hat{W}_1, \hat{W}_2) = g(\mathbf{I}_1, \mathbf{I}_2, T^n)$, where we define $\mathbf{I}_1 \triangleq I_1(1), \ldots, I_1(M_1)$, and $\mathbf{I}_2 \triangleq I_2(1), \ldots, I_2(M_2)$.

The average error probability in the identification process is defined as

$$P_e^n \triangleq \frac{1}{M_1 M_2} \sum_{(w_1,w_2)} \Pr[(\hat{W}_1,\hat{W}_2)\neq(W_1,W_2)|(W_1,W_2)=(w_1,w_2)].$$

Definition 1: $(R_1^c, R_2^c, R_1^i, R_2^i)$ is an *achievable* compresion/identification rate tuple for a parent identification system if, for any $\epsilon > 0$ and sufficiently large n, there exist deterministic enrollment functions f_1 and f_2 and a deterministic identification function g such that

$$\frac{1}{n}\log L_j \leq R_j^c \text{ and } \frac{1}{n}\log M_j \geq R_j^i, \text{ for } j = 1, 2, \quad (3)$$

and $P_e^n \leq \epsilon$.

Definition 2: The capacity region $\mathcal{R}$ for a parent identification system is the set of all achievable rate tuples $(R_1^c, R_2^c, R_1^i, R_2^i)$.

III. Main Result

In this section, we provide single-letter inner and outer bounds on the achievable rate region. These two bounds do not match in general, and the capacity region for the parent identification problem is still open. As is common for many multi-user information theory problems, the bounds are expressed in terms of auxiliary random variables U_1 and U_2, which are defined over finite alphabet sets $\mathcal{U}_1$ and $\mathcal{U}_2$, respectively. For a given joint distribution $P_{X_1,X_2,Y_1,Y_2,Z,T}$ that is in the form of (2), we define two different sets:

$$\begin{aligned}\mathcal{P}_{in} \triangleq \{(U_1,U_2) \quad : \quad & P_{U_1,U_2X_1,X_2,Y_1,Y_2,Z,T} = \\ & P_{U_1|Y_1}P_{U_2|Y_2}P_{X_1,X_2,Y_1,Y_2,Z,T}\},\end{aligned}$$

and

$$\begin{aligned}\mathcal{P}_{out} \triangleq \{(U_1,U_2) \quad : \quad & U_1 - Y_1 - X_1 - Z - T, \\ & U_2 - Y_2 - X_2 - Z - T\}.\end{aligned}$$

The set $\mathcal{P}_{in}$, in addition to the two Markov chain constraints in $\mathcal{P}_{out}$, has the additional constraint that (U_1, Y_1, X_1) is independent of (U_2, Y_2, X_2).

For a given pair of auxiliary random variables (U_1, U_2) jointly distributed with X_1, X_2, Y_1, Y_2, Z, T, we define the following rate region:

$$\begin{aligned}\mathcal{R}_{U_1,U_2} = \{(R_1^c, R_2^c, R_1^i, R_2^i) \quad : \quad & R_1^c \geq I(U_1;Y_1), \\ & R_2^c \geq I(U_2;Y_2), \\ & R_1^i \leq I(U_1;T|U_2), \\ & R_2^i \leq I(U_2;T|U_1) \text{ and} \\ & R_1^i + R_2^i \leq I(U_1,U_2;T)\}.\end{aligned}$$

Single letter bounds on $\mathcal{R}$ are given in the following theorem, whose proof can be found in Section IV.

Theorem 1: $\bar{\mathcal{R}}_{in} \subseteq \mathcal{R} \subseteq \bar{\mathcal{R}}_{out}$, where we define

$$\begin{aligned}\mathcal{R}_{in} \triangleq & \{(R_1^c, R_2^c, R_1^i, R_2^i) : (R_1^c, R_2^c, R_1^i, R_2^i) \in \mathcal{R}_{U_1,U_2} \\ & \text{for } (U_1,U_2) \in \mathcal{P}_{in}\}, \text{ and} \quad (4) \\ \mathcal{R}_{out} \triangleq & \{(R_1^c, R_2^c, R_1^i, R_2^i) : (R_1^c, R_2^c, R_1^i, R_2^i) \in \mathcal{R}_{U_1,U_2} \\ & \text{for } (U_1,U_2) \in \mathcal{P}_{out}\}, \quad (5)\end{aligned}$$

and $\bar{A}$ denotes the convex hull of the set A.

Corollary 1: If $R_j^c = H(Y_j)$ for $j = 1, 2$, then the two bounds match and the identification rate region is characterized as the rate pairs (R_1^i, R_2^i) satisfying

$$\begin{aligned}R_1^i &\leq I(Y_1;T|Y_2), \\ R_2^i &\leq I(Y_2;T|Y_1) \text{ and} \\ R_1^i + R_2^i &\leq I(Y_1,Y_2;T)\}.\end{aligned}$$

If we are interested in identifying a single parent, e.g., the case of asexual reproduction, the problem reduces to finding the rate region for compression and identification for a single database, i.e., $\mathcal{X}_2 = \mathcal{Y}_2 = \emptyset$. In this case, we have a single Markov chain and the upper and lower bounds match, and we recover the rate region obtained in [3], [4]:

Corollary 2: The compression/identification rate region for a single database system is the union of all rate pairs (R_1^c, R_1^i) satisfying

$$R_1^c \geq I(U_1;Y_1) \text{ and } R_1^i \leq I(U_1;T)$$

for some auxiliary random variable U_1 such that $U_1 - Y_1 - X_1 - Z - T$ forms a Markov chain.

Remark 1: It is pointed out in [6] that the capacity/storage tradeoff problem (or, the pattern recognition problem as stated in [3]) for a single database as in Corollary 2 is inherently related to the information bottleneck (IB) method introduced in [7]. Hence, the solution of the IB problem also constitutes a solution for the rate region in Corollary 2. However, this equivalence is established based on the single-letter characterization of the capacity region. For identification over multiple databases we do not have a capacity characterization. On the other hand, we can identify an equivalent multivariate IB problem [8] for the achievable rate region. Hence, we can use the algorithms proposed for the multivariate IB problem in [8] to numerically evaluate these regions.

IV. Proof of Theorem 1

We start with the proof of the inner bound, that is, $\bar{\mathcal{R}}_{in} \subseteq \mathcal{R}$. We assume that $(R_1^c, R_2^c, R_1^i, R_2^i) \in \mathcal{R}_{in}$. Fix any $\epsilon > 0$.

Codebook generation: For database $j = 1, 2$, generate a codebook consisting of L_j length-n codewords i.i.d. with distribution p_{U_j}. Enumerate these codewords as $U_j^n(l_j)$ where $l_j \in \{1, \ldots, L_j\}$. We will determine L_j later.

Enrollment: Given the noisy observation of a feature vector $y_j^n \in \mathcal{Y}_j^n$, define the enrollment function f_j as the smallest index l_j such that $(y_j^n, U_j^n(l_j)) \in T^n_{[U_jY_j]_\epsilon}$[1]. We set $f_j(y_j^n) = 1$ if no such codeword exits.

Identification: In the identification phase, given any $t^n \in \mathcal{T}^n$, $\mathbf{I}_1$, and $\mathbf{I}_2$, we define the identification function g as the smallest pair of indices w_1 and w_2 such that $(t^n, U_1^n(I_1(w_1)), U_2^n(I_2(w_2))) \in T^n_{[TU_1U_2]_\epsilon}$. We set $g(t^n, \mathbf{I}_1, \mathbf{I}_2) = (1, 1)$ if no such pair can be found. We define $(\hat{w}_1, \hat{w}_2) = g(t^n, \mathbf{I}_1, \mathbf{I}_2)$.

Probability of Error Analysis: Define the following events

$$E_{1j}(w_j) \triangleq \left\{ \left(Y_j^n(w_j), U_j^n(I_j(w_j))\right) \in T^n_{[U_jY_j]_\epsilon} \right\}$$

[1]We use strong typicality arguments in the proof, where the set of all x^n strongly ϵ-typical with X is denoted by $T^n_{[X]_\epsilon}$. See [9] for further details.

for $j = 1, 2$, and

$$E_2(w_1, w_2) \triangleq \left\{ \left(T^n, U_1^n(I_1(w_1)), U_2^n(I_2(w_2))\right) \in T^n_{[TU_1U_2]_\epsilon} \right\}.$$

The probability of error can be bounded as follows:

$$\begin{aligned} P_e^n &\le P[E_{11}^c(w_1)] + P[E_{12}^c(w_2)] \\ &\quad + P[E_2^c(w_1, w_2)|E_{11}(w_1), E_{12}(w_2)] \\ &\quad + \sum_{m_1 \neq w_1} P[E_2(m_1, w_2)] + \sum_{m_2 \neq w_2} P[E_2(w_1, m_2)] \\ &\quad + \sum_{m_1 \neq w_1, m_2 \neq w_2} P[E_2(m_1, m_2)]. \end{aligned}$$

It is easy to see that $P[E_{1j}^c(w_j)]$, $j = 1, 2$, can be made arbitrarily small for a sufficiently large n if

$$\frac{1}{n} \log L_j \ge I(U_j; Y_j) + \frac{\epsilon}{2};$$

hence we set $L_j = 2^{n(R_j^c + \epsilon)}$. Similarly, we can also let $P[E_2^c(w_1, w_2)|E_{11}(w_1), E_{12}(w_2)]$ go to zero for sufficiently large n which follows from the Markov Lemma [10].

We also have,

$$\sum_{m_1 \neq w_1} P[E_2(m_1, w_2)] \le M_1 2^{-n(I(T;U_1|U_2) - \frac{\epsilon}{2})}, \quad (6)$$

which can be made arbitrarily small for sufficiently large n if,

$$\frac{1}{n} \log M_1 \le I(T; U_1|U_2) - \epsilon \le R_1^i - \epsilon. \quad (7)$$

Similarly, we also need

$$\frac{1}{n} \log M_2 \le I(T; U_2|U_1) - \epsilon \le R_2^i - \epsilon. \quad (8)$$

Finally, for the last term in the error probability bound

$$\sum_{m_1 \neq w_1, m_2 \neq w_2} P[E_2(m_1, m_2)] \le M_1 M_2 2^{-n(I(T;U_1,U_2) - \frac{\epsilon}{2})}, \quad (9)$$

can be made arbitrarily small for sufficiently large n if,

$$\tfrac{1}{n}(\log M_1 + \log M_2) \le I(T; U_1, U_2) - \epsilon \le R_1^i + R_2^i - \epsilon. \quad (10)$$

Since we can choose M_1 and M_2 such that (7), (8) and (10) are all satisfied, we have shown that $P_e^n \to 0$ as $n \to \infty$.

This proves that the average probability of error, averaged over the ensembles of codebooks, can be made arbitrarily small given $(R_1^c, R_2^c, R_1^i, R_2^i) \in \mathcal{R}_{in}$. Hence, there exists at least one code with arbitrarily small average probability of error. The convex hull $\bar{\mathcal{R}}_{in}$ is achieved based on the usual time-sharing arguments.

Next, we prove the outer bound, that is, $\mathcal{R} \subseteq \mathcal{R}_{out}$. Assume that $(R_1^c, R_2^c, R_1^i, R_2^i) \in \mathcal{R}$. Then, for any $\epsilon > 0$ and sufficiently large n, there exist enrollment and identification functions f_1, f_2 and g such that

$$L_j \le 2^{nR_j^c} \text{ and } M_j \ge 2^{nR_j^i}, \quad (11)$$

for $j = 1, 2$, and $P_e^n < \epsilon$. We have

$$\begin{aligned} \log M_1 &= H(W_1|\mathbf{I}_1, \mathbf{I}_2, T^n) + I(W_1; \mathbf{I}_1, \mathbf{I}_2, T^n) && (12) \\ &\le H(W_1|\hat{W}_1) + I(W_1; \mathbf{I}_1, \mathbf{I}_2, T^n) && (13) \\ &\le 1 + P_e^n \log M_1 + I(W_1; \mathbf{I}_1, \mathbf{I}_2, T^n) && (14) \end{aligned}$$

where (13) follows since $\hat{W}_1$ is a deterministic function of $\mathbf{I}_1, \mathbf{I}_2$ and T^n; (14) follows from Fano's inequality. From here we can obtain

$$\begin{aligned} (1-\epsilon) \log M_1 - 1 &\le I(W_1; \mathbf{I}_1, \mathbf{I}_2, T^n) && (15) \\ &= I(W_1; T^n|\mathbf{I}_1, \mathbf{I}_2) && (16) \\ &= H(W_1|\mathbf{I}_1, \mathbf{I}_2) - H(W_1|\mathbf{I}_1, \mathbf{I}_2, T^n) && (17) \\ &\le H(W_1|\mathbf{I}_1, \mathbf{I}_2, W_2) - H(W_1|\mathbf{I}_1, \mathbf{I}_2, T^n, W_2) && (18) \\ &= I(W_1; T^n|W_2, \mathbf{I}_1, \mathbf{I}_2) && (19) \\ &\le H(T^n|W_2, \mathbf{I}_2) - H(T^n|W_1, W_2, \mathbf{I}_1, \mathbf{I}_2) && (20) \\ &= H(T^n|I_2(W_2)) - H(T^n|I_1(W_1), I_2(W_2)) && (21) \end{aligned}$$

where (16) follows since W_1 is independent of the database entries $(\mathbf{I}_1, \mathbf{I}_2)$; (18) follows since W_1 is independent of W_2 and conditioning reduces entropy; and (21) follows since T^n is independent of $I_1(m_1)$ with $m_1 \neq W_1$ and $I_2(m_2))$ with $m_2 \neq W_2$.

We define, for $j = 1, 2$, $U_{j,i} \triangleq (T^{i-1}, I_j(W_j))$. Using this definition and (11), we obtain

$$\begin{aligned} (1-\epsilon) n R_1^i - 1 &\le H(T^n|I_2(W_2)) - H(T^n|I_1(W_1), I_2(W_2)) \\ &= \sum_{i=1}^n \big[H(T_i|T^{i-1}, I_2(W_2)) \\ &\qquad - H(T_i|T^{i-1}, I_1(W_1), I_2(W_2)) \big] && (22) \\ &\le \sum_{i=1}^n \left[H(T_i|U_{2,i}) - H(T_i|U_{1,i}, U_{2,i}) \right] && (23) \\ &= \sum_{i=1}^n \left[I(T_i; U_{1,i}|U_{2,i}) \right]. && (24) \end{aligned}$$

Hence, we have, for $(j, k) \in \{(1, 2), (2, 1)\}$

$$(1-\epsilon) R_j^i \le \frac{1}{n} \sum_{i=1}^n \left[I(T_i; U_{j,i}|U_{k,i}) \right] + \frac{1}{n}. \quad (25)$$

For the total rate of identification we have

$$\begin{aligned} \log M_1 M_2 &= H(W_1, W_2) && (26) \\ &= H(W_1, W_2|\mathbf{I}_1, \mathbf{I}_2, T^n) + I(W_1, W_2; \mathbf{I}_1, \mathbf{I}_2, T^n) && (27) \\ &\le H(W_1, W_2|\hat{W}_1, \hat{W}_2) + I(W_1, W_2; \mathbf{I}_1, \mathbf{I}_2, T^n) && (28) \\ &\le 1 + P_e^n \log M_1 M_2 + I(W_1, W_2; \mathbf{I}_1, \mathbf{I}_2, T^n) && (29) \end{aligned}$$

where (29) follows from Fano's inequality. Then, we can write

$$\begin{aligned} (1-\epsilon) \log M_1 M_2 - 1 &\le I(W_1, W_2; \mathbf{I}_1, \mathbf{I}_2, T^n) && (30) \\ &= I(W_1, W_2; T^n|\mathbf{I}_1, \mathbf{I}_2) && (31) \\ &\le H(T^n) - H(T^n|W_1, W_2, \mathbf{I}_1, \mathbf{I}_2) && (32) \\ &= H(T^n) - H(T^n|I_1(W_1), I_2(W_2)) && (33) \\ &= \sum_{i=1}^n \big[H(T_i|T^{i-1}) - H(T_i|T^{i-1}, I_1(W_1), I_2(W_2)) \big] \\ &\le \sum_{i=1}^n \left[H(T_i) - H(T_i|U_{1,i}, U_{2,i}) \right] && (34) \\ &= \sum_{i=1}^n \left[I(T_i; U_{1,i}, U_{2,i}) \right]. && (35) \end{aligned}$$

where (31) follows since W_1 and W_2 are independent of the database entries $(\mathbf{I}_1, \mathbf{I}_2)$; and (33) follows since T^n is independent of $I_1(m_1)$ with $m_1 \neq W_1$ and $I_2(m_2)$ with $m_2 \neq W_2$. Finally, we can obtain

$$(1-\epsilon)(R_1^i + R_2^i) \leq \frac{1}{n}\sum_{i=1}^{n}[I(T_i; U_{1,i}, U_{2,i})] + \frac{1}{n}. \quad (36)$$

We need to show that $U_{1,i}$ and $U_{2,i}$ satisfy the Markov chains in the outer bound. We show that $U_{1,i} - Y_{1,i}(W_1) - X_{1,i}(W_1) - Z_i - T_i$ form a Markov chain. Since we already know that $Y_{1,i}(W_1) - X_{1,i}(W_1) - Z_i - T_i$ and $U_{1,i} - Y_{1,i}(W_1) - X_{1,i}(W_1)$ form Markov chain relationships, it is sufficient to show that $U_{1,i} - (Y_{1,i}(W_1), X_{1,i}(W_1)) - Z_i$ and $U_{1,i} - (Y_{1,i}(W_1), X_{1,i}(W_1), Z_i) - T_i$ form two Markov chains.

$$\begin{aligned}
I(U_{1,i}; Z_i | Y_{1,i}(W_1), X_{1,i}(W_1)) &= H(U_{1,i}|Y_{1,i}(W_1), X_{1,i}(W_1)) \\
&\quad - H(U_{1,i}|Y_{1,i}(W_1), X_{1,i}(W_1), Z_i), \\
&= H(T^{i-1}, I_1(W_1)|Y_{1,i}(W_1), X_{1,i}(W_1)) \\
&\quad - H(T^{i-1}, I_1(W_1)|Y_{1,i}(W_1), X_{1,i}(W_1), Z_i), \\
&= H(T^{i-1}|Y_{1,i}(W_1), X_{1,i}(W_1)) \\
&\quad + H(I_1(W_1)|T^{i-1}, Y_{1,i}(W_1), X_{1,i}(W_1)) \\
&\quad - H(T^{i-1}|Y_{1,i}(W_1), X_{1,i}(W_1), Z_i) \\
&\quad - H(I_1(W_1)|T^{i-1}, Y_{1,i}(W_1), X_{1,i}(W_1), Z_i), \\
&= H(I_1(W_1)|T^{i-1}, Y_{1,i}(W_1), X_{1,i}(W_1)) \\
&\quad - H(I_1(W_1)|T^{i-1}, Y_{1,i}(W_1), X_{1,i}(W_1), Z_i), \\
&= 0, \quad (37)
\end{aligned}$$

where the last equality follows since $T_i - Z_i - (X_{1i}, Y_{1,i}, T^{i-1}) - I_1(W_1)$. Similarly, it can be shown that $I(U_{1,i}; T_i | Y_{1,i}(W_1), X_{1,i}(W_1), Z_i) = 0$.

Next, we bound the enrollment rates. For $j = 1, 2$, we have the following:

$$\begin{aligned}
nR_j^c &\geq \log L_j \\
&\geq H(I_j(W_j)) \\
&= H(I_j(W_j)) - H(I_j(W_j)|Y_j^n(W_j)) \\
&= I(I_j(W_j); Y_j^n(W_j)) \\
&= H(Y_j^n(W_j)) - H(Y_j^n(W_j)|I_j(W_j)) \\
&= \sum_{i=1}^{n}\left[H(Y_{j,i}(W_j)) - H(Y_{j,i}(W_j)|Y_j^{i-1}, I_j(W_j))\right] \\
&= \sum_{i=1}^{n}\left[H(Y_{j,i}(W_j)) - H(Y_{j,i}(W_j)|Y_j^{i-1}, I_j(W_j), T^{i-1})\right] \quad (38) \\
&\geq \sum_{i=1}^{n}\left[H(Y_{j,i}(W_j)) - H(Y_{j,i}(W_j)|I_j(W_j), T^{i-1})\right] \\
&\geq \sum_{i=1}^{n} I(Y_{j,i}(W_j); U_{j,i})
\end{aligned}$$

where (38) follows from the fact that $Y_{j,i}(W_j) - (Y_j^{i-1}, I_j(W_j)) - T^{i-1}$ forms a Markov chain.

Next, we introduce a time-sharing random variable Q independent of all the other random variables of interest and uniformly distributed over $\{1, \ldots, n\}$. We can rewrite (25) as

$$\begin{aligned}
(1-\epsilon)R_1^i &\leq [I(T_Q; U_{1,Q}|U_{2,Q}, Q)] + \frac{1}{n}. \\
&= [I(T; U_1|U_2, Q)] + \frac{1}{n},
\end{aligned}$$

where we defined the new random variables as $T \triangleq T_Q$, $U_1 \triangleq U_{1,Q}$ and $U_2 \triangleq U_{2,Q}$. Following similar steps to those for (36) and letting $n \to \infty$ and $\epsilon \to 0$, we obtain

$$R_1^i \leq I(T; U_1|U_2, Q), \quad (39a)$$

$$R_2^i \leq I(T; U_2|U_1, Q) \text{ and} \quad (39b)$$

$$R_1^i + R_2^i \leq I(T; U_1, U_2|Q). \quad (39c)$$

Also defining $Y_1 \triangleq Y_{1,Q}$ and $Y_2 \triangleq Y_{2,Q}$, we obtain

$$R_1^c \geq I(Y_1; U_1, |Q) \text{ and} \quad (40a)$$

$$R_2^c \geq I(Y_2; U_2, |Q). \quad (40b)$$

It is possible to show that the set of rate points satisfying (39) and (40) is equivalent to $\bar{\mathcal{R}}_{out}$.

V. Conclusions

We have studied the tradeoff between the storage and the identification rates over multiple databases. We have considered the joint identification of ancestors over two separate databases, which consist of the compressed noisy observations of the data vectors. We have presented single-letter inner and outer bounds on the set of achievable rate points, which identify a tradeoff between the compression rates and the identification rate region; the lower the compression rates for the enrollment process, the larger the identification rate region.

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